SEQ ID NO:1

GCCCTGCCTGCCCTGCCTGCCCTGCCTGCCCTGCCTGCCCTGCCTGCCCTGCCTGCCCTGCCTGCC
CTGCCTCAGGAATCCCAGAACGAAGGCCTGGCCTGGGCCTTCCTGGCCATGGCTCCCTCAGTCCTCTGGGCACCA
CAAAGGCTTTTTCCCAGGAAGAGAACGCCTTGCCTCTACTTGTAGCTGGGGTTGCCTGGGAGGTGCGTCATAGTG
TGTCTTAGTAAGTTTTGAACACTGGGGAAGAGCCTCAGGCGTCTCTACGCGGGTAGTGTCAGTGCTGACCCTTTG
AAAGTGGTGTGTTCCCTTCTGAGGGATGTGCCTGTGGTGAACTCTTCAGGAGAGCTGCCCCAGGGAAGGACAGGA
CAGATGTCTTTTAAACACCAGGGAAAGTACACAGCCTCCCGCCTCAGGCGGAGCCCAGTGGAAAGTAGCCACCTT
CCTTGCAATCTGCCACACCTGGCACAGGAGAGCCTGCACTGGCCGCGTTGGGCTTTGGTGCTGGCTCTGTACTCC
CACTTGCTTGCTGGTGGCCTCANGGAAAGGTCATCTCTNAANGAAACAAAGCCACCTNCTCCCCCTCCCTGGCAT
GCNTTTTTCNGCCCACAGCCCCGTGTGTGCCAACANAAATTTTGGCNNCANGANGNAAGGNTGGGANANAACCCN
AAAACTATTGTGGCTNCCCTGTTGCCCCTGCTGTNCCNGGTTTNATGGGAACGAGGNCCTCCCACCCCCTNGGNA
ACGNATAACCNCACCCGTGGNAATGGNGGGNTTGGGGTGCANTCNTTACCCNCCCCANGGGNNAGGGCGGGGGNT
CAAACCTNGGGGAACNNAAAAAAAAAACCCANGGCCNTTTGNGTCCNCNNNGGCCCCNAGGGNTTTTATTTTNTTT
ANAANGGGANGGTGNCCCCAATNCTCNNAAAACTNGGNTTTTTTAAGNNTTTCTTGCAAAATTGNN

**FIG. 1A**

```
3        824   ---CTTCTCTGCACTTCTATGGATAGAACTTTCAA---CGAACCCAGCTATTTAGTGGTCG
4        275   TGACTTCGCGCTGCACCTA---ACAGACCTTGAAACAGGAACCCAGCTATTTAGTGGTCG
2          1   ------------------------------------------------------------
1        251   CGACTTTGCGCTGCACCTA---ACAGACCTTGAAACAGGAACCCAGCTGTTTAGTGGTCA
consensus 841   ...................          .........................
```

```
3        879   AAGTGACTTTAGAATCACTACCTTGAAATTCCATCCAAAAGACCACAACATCTTTTTATG
4        332   AAGTGACTTTAGAATCACTACCTTGAAATTCCATCCAAAAGACCACAACTCTTTTTATG
2          1   ------------------------------------------GTCTTTT-ATG
1        308   GAGTGACTTCAGAGTCACCACCTTGAAATTTCATCCAAAAGAACACAACGTCTTTT----
consensus 901   .........................................******......
```

```
3        939   TGGAGGCTTCAGCTCTGAAATGAAAGCTTGGGATATAAGGACTGGCAAGGTGATGAGAAG
4        392   TGGAGGCTTCAGCTCTGAAATGAAAGCTTGGGATATAAGGACTGGCAAGGTGATGAGAAG
2         11   TGGCGGCTTCAGCTCTGAAATCAACGGGNGGGACATGAGGACTGGCAAGGTGGTGAAAGG
1              ------------------------------------------------------------
consensus 961   ....................................................
```

```
3        999   CTACAAGGCGACCATCCAGCAGACCTTGGACATCCTGTTCCTCCGGGAAGGCTCCGAGTT
4        452   CTACAAGGCGACCATCCAGCAGACCTTGGACATCCTGTTCCTCCGGGAAGGCTCCGAGTT
2         71   CTACAAGGCCACCATCCAGCAGACCTGGACATTCTCTTCCTCCAGGAGGGCTCCGAGTT
1              ------------------------------------------------------------
consensus 1021  .....................................................
```

```
3       1059   CCTGAGCAGCACAGACGCTTCCACCCGGGACTCAGCTGACCGCACCATTATTGCCTGGGA
4        512   CCTGAGCAGCACAGACGCTTCCACCCGGGACTCAGCTGACCGCACCATTATTGCCTGGGA
2        131   TCTTAGCAGTACGGACGGCATCCACCCGGGACTCTGCTGACCGAACCATTATCGCCTGGGA
1              ------------------------------------------------------------
consensus 1081  .....................................................
```

```
3       1119   TTTCCGGACCTCTGCCAAAATCTCCAACCAGATTTTCCACGAGAGGTTCACCTGCCCCAG
4        572   TTTCCGGACCTCTGCCAAAATCTCCAACCAGATTTTCCACCTGCCCCAG
2        191   TTTCCGGACCGCTGCCAAGATCTCCAACCAGATCTTCCATGAGAGGTACACCTGTGCCCAG
1              ------------------------------------------------------------
consensus 1141  .....................................................
```

```
3       1179   CCTCGCCTTGCACCCGAGAGAGCCCGTGTTCCTGGCACAGACCAATGGCAACTACCTGGC
4        632   CCTCGCCTTGCACCCGAGAGAGCCCGTGTTCCTGGCACAGACCAATGGCAACTACCTGGC
2        251   CCTCGCCTTGCATCCAAGGGAGCTGTGTTCCTGGCACAAACCAATGGCAACTACCTGGC
1              ------------------------------------------------------------
consensus 1201  .....................................................
```

```
3       1239   CCTTTTCTCCACTGTGTGGCCCTACCGGATGAGCAGACGGCGGCGCTATGAAGGGCACAA
4        692   CCTTTTCTCCACTGTGTGGCCCTACCGGATGAGCAGACGGCGGCGCTATGAAGGGCACAA
2        311   TCTCTTTTGCTGTGTGTGGCCCTATCGGATGAGCAGACGGABACGCTACGAAGGTCACAA
1              ------------------------------------------------------------
consensus 1261  .....................................................
```

```
3       1299   GGTGGAGGGCTACTCAGTGGGCTGCGAGTGCTCCCCAGGCGGTGACTTGCTGGTGACGGG
4        752   GGTGGAGGGCTACTCAGTGGGCTGCGAGTGCTCCCCAGGCGGTGACTTGCTGGTGACGGG
2        371   GGTGGAAGGCTACGCGGTGGGCTGTCACTCTTCCCCATCTGCTGACCTGCTGCTGACAGG
1              ------------------------------------------------------------
consensus 1321  .....................................................
```

```
3       1359   CAGCGCCGATGGCCGGGTCCTGATGTACAGCTTCCGCACAGCCCAGCCGAGCATGCACACT
4        812   CAGCGCCGATGGCCGGGTCCTGATGTACAGCTTCCGCACAGCCCAGCCGAGCATGCACACT
2        431   CAGCGCTGATGGCCGGGTTTTGATGTACAGTTTCCGCACGGCCAGCCGAGCGTGCGCACT
1              ------------------------------------------------------------
consensus 1381  .....................................................
```

```
3       1419   GCAGGGGCACACACAGGCCTGTGTCGGCACCACCTATCACCCCGTGCTGCCCTCCGTCCT
4        872   GCAGGGGCACACACAGGCCTGTGTCGGCACCACCTACCACCCCGTGCTGCCCTCCGTCCT
2        491   ACAAGGGCACACGCAGGCCTGCCTTGGCACCAGCTACCATCCTGTGCTGCCGTTCTGTCCT
1              ------------------------------------------------------------
consensus 1441  .....................................................
```

```
3       1479   CGCCACCTGCTCCTGGGGAGGGGACATGAAGATCTGGCACTGAGCTTTTTGTCACTGAAC
4        932   CGCCACCTGCTCCTGGGGAGGGGACATGAAGATCTGGCACTGAGCTTTTTGTCACTGAAC
2        551   CGGCACCTGCTCCTGGGGAGGAGACATCAAGATCTGGCACT--------------AAC
1              ------------------------------------------------------------
consensus 1501  .....................................................
```

**FIG. 1B**

```
3         1539  CTTCCCGATGCCAGCTGGGCTCTTGGACTCCCCTCTTCCTCAAGGGTAGATGAGAGGAAC
4          992  CTTCCCGATGCCAGCTGGGCTCTTGGACTCCCCTCTTCCTCAAGGGTAGATGAGAGGAAC
2          595  -------TGGCAACTGAGACCTG-----CCCCT----------GGG------ATAGG--C
1               ------------------------------------------------------------
consensus 1561  ............................................................


3         1599  GAGCACAGAGGTT-GGCTGTGGGTCCTGGGTACCACCTTCTGAGCCTCAGTTTCCTCATC
4         1052  GAGCACAGAGGTT-GGCTGTGGGTCCTGGGTACCACCTTCTGAGCCTCAGTTTCCTCATC
2          625  G-GC-CGGAGGTCACGGCTGC---TCCCGAG---AGCTGCTGGGCTTCAGTGACC-TCGGC
1               ------------------------------------------------------------
consensus 1621  ...........................................................


3         1658  TGTAAAGTGGGGA-GAAAAGTCTGTTT-GCCTCAGGAGTGTG--AGGACTACACTAGTGA
4         1111  TGTAAAGTGGGGA-GAAAAGTCTGTTT-GCCTCAGGAGTGTG--AGGACTACACTAGTGA
2          675  TATAGCATGGGGGTGAGAACCGCGTCTCGGCGCAAGCCTGTGTCAGAACGGGG-TAGCCG
1               ------------------------------------------------------------
consensus 1681  ...........................................................


3         1714  AAGCGCCTGGCGGGCAGCCGGCGATGCCCAATAAATGTGTGTTTGCTGTTTGTTAAAAA
4         1167  AAGCGCCTGGCGGGCAGCCGGCGATGCCCAATAAATGTGTGTTTGCTGTTTGTTAAAAA
2          734  AAGTGACTGGTGGGCGA--------------------------------------------
1               ------------------------------------------------------------
consensus 1741  ...........................................................
```

FIG. 1B (continued)

SEQ ID NO:2

GAGGGGTGGACCAAGAGCTTCCGTGTGTGTGTGTGTGTGGAAGTCACCTTTGTGTGACTGTATGGCCTCGCTGGT
GGCATATGATGATTCTGACTCCGAGACCGAGGCTGACCCTGCCAGAAGTGGGGACGCTGCAGGTGTGGAATGCTG
TGGACTCGGGACACTGCCTGCAGACCTACTCTGTGCACAGTGAGGCAGTAAGGGCTGAACGGTGGTCTCCCTGTG
GCCGGCGCATCCTCAGTGGTGGCTTCGACTTTGCCCTGCACCTAACAGACCTTGAAACAGGAACCCAAGTGTTTA
GTGGTCAGAGTGACTTCAGAGTCACCACCTTGAAATTTCATCCAAAAGAACACAACGTCTTTTtATGTGGCGGCT
TCAGCTCTGAAATCAACAGGNGGGACATGAGGACTGGCAAGGTGGTGAAAGGCTACAAGGCCACCATCCAGCAGA
CCCTGGACATTCTCTTCCTCCAGGAGGGCTCCGAGTTTCTTAGCAGTACGGACGCATCCACCCGGGACTCTGCTG
ACCGAACCATTATCGCCTGGGATTTCCGGACCGCTGCCAAGATCTCCAACCAGATCTTCCATGAGAGGTACACCT
GTCCCAGCCTCGCCTTGCATCCAAGGGAGCCTGTGTTCCTTGCACAAACCAATGGCAACTACCTGGCTCTCTTTT
CCTCTGTGTGGCCCTATCGGATGAGCAGACGGAGACGCTACGAAGGTCACAAGGTGGAAGGCTACGCGGTGGGCT
GTGAGTGTTCCCCATGTGGTGACCTGCTGGTGACAGGCAGCGCTGATGGCCGGGTTTTGATGTTCAGTTTCCGCA
CGGCCAGCCGAGCGTGCGCACTACAAGGGCACACGCAGGCCTGCCTTGGCACCAGCTACCATCCTGTGCTGCCTT
CTGTCCTCGGGACCTGCTCCTGGGGAGGAGACATCAAGATCTGGCACTAACTGGCAACTGAGACCTGCCCCTGGG
ATAGGCGGCCGGAGGTCAGGCTGCTCCCGAGAGCTGCTGGGCTTCAGTGACTCGGCTATAGCATGGGGGTGAGAA
CGCCGTCTCGGCGCAAGCGTGTGTCAGAACGGGGTAGCCGAAGTGACTGGTGGGCGA

**FIG. 2A**

SEQ ID NO:3

MMILTPRPRLTLPEVGTLQVWNAVDSGHCLQTYSVHSEAVRAERWSPCGRRILSGGFDFALHLTDLETGTQVFSG
QSDFRVTTLKFHPKEHNVFLCGGFSSEINRXDMRTGKVVKGYKATIQQTLDILFLQEGSEFLSSTDASTRDSADR
TIIAWDFRTAAKISNQIFHERYTCPSLALHPREPVFLAQTNGNYLALFSSVWPYRMSRRRRYEGHKVEGYAVGCE
CSPCGDLLVTGSADGRVLMFSFRTASRACALQGHTQACLGTSYHPVLPSVLGTCSWGGDIKIWH

**FIG. 2B**

Exon 1
SEQ ID NO:4

```
ATGACAGGCTGGGTGGGCGGCGCCGCCGCAGCCTCCCGGTCCCTCGTGGT
ACAGGTGCCCAGAGAACAGACAGCCCGGTTCCGAGCTGGATCCTCGGGGC
GCGGCGCCGGGGCGTCAACCGAAGGCCCCGGCGCCACCTCGGCATCCCTC
CCTCGCTCCCGGCGCAGTGACCACCCCCTCCTCACTTACCGGCGGCCCCC
ACTTCGGCCCCACCAGTCAGCACCCCCAAGTTCAGCCACCGGTACCTCTT
GGGCGTCCGTGGAAACACCAGCCGGCTGGAATAACTTCCG
```

Exon 2
SEQ ID NO:5

```
GAAGTCACCTTTGTGTGACTGTATGGCCTCGCTGGTGGCATATGATGATT
CTGACTCCGAGACCGAGGCTGACCCTGCCAGAAGTGGGGACGCTGCAG
```

Exon 3
SEQ ID NO:6

```
CTGCCTGTCTTAAGCCACTAAAACCTGCCTGG
GACGTCCTCAAACCTTCTCATGATCAAAGCACATTTGAAAGCACAGCTGG
AAATGCCAGCTCTTCTCAGAGGAAAAGGGGTGAGGACTGTGTGCTTCCCT
ATATCCCCAAGAGGCTAAGGCAGCTGCAAGCGCTGAATCCAGAAGCAG
```

Exon 4
SEQ ID NO:7

```
TGTCTGAGTTCATCCAGCCATATTTGA
ACAGTCAGTACAGAGAGACTACGGTCCCCAAGAAAGTGCTTTTCCACCTT
CGAGGCCACAGGGGCCCGGTCAACAGCATTCAGTGGTGTCCAGTCTTTTG
CAAGAGCCACATGCTTCTCTCTGCTTCCATGGACAAAACCTTCAAG
```

Exon 5
SEQ ID NO:8

```
TTCTGCCGTGAACATGGCTATGCA
GGCACCTCTGTGGATCCCGACACAGGCTCCTTTGGGATGGACCCAG
```

Exon 6
SEQ ID NO:9

```
GAATCC
CAGAACGAAGGCCTGGCCTGGGCCTTCCTGGCCATGGCTCCCTCAGTCCT
CTGGGCACCACAAAGGCTTTTTCCCAGGAAGAGAACGCCTTGCCTCTACT
TGTAGCTGGGGTTGCCTGGGAG
```

FIG. 2C

SEQ ID NO:10
ggcacgagggagggaggaggtgagagtgattagtgggagaagaaaagcaggcccaggaccaagccctggggactg
gggacatcctcggtgaccctgtggagcattgagccatgccagctctgtgcctggtgctgtgctggtttcaagggc
tgttgggagaggtatggaacgccgtggactccgggcactgcctgcagacctactccctgcacacagaggcagtgc
gggccgccggtgggctccctgtggccggcgcatcctcagtggtggctttgacttcgcgctgcacctaacagacc
ttgaaacaggaacccagctatttagtggtcgaagtgactttagaatcactaccttgaaattccatccaaaagacc
acaacatcttttatgtggaggcttcagctctgaaatgaaagcttgggatataaggactggcaaggtgatgagaa
gctacaaggcgaccatccagcagaccttggacatcctgttcctccgggaaggctccgagttcctgagcagcacag
acgcttccacccgggactcagctgaccgcaccattattgcctgggatttccggacctctgccaaaatctccaacc
agattttccacgagaggttcacctgccccagcctcgccttgcacccgagagagcccgtgttcctggcacagacca
atggcaactacctggcccttttctccactgtgtggccctaccggatgagcagacggcggcgctatgaagggcaca
aggtggagggctactcagtgggctgcgagtgctccccaggcggtgacttgctggtgacgggcagcgccgatggcc
gggtcctgatgtacagcttccgcacagccagccgagcatgcacactgcaggggcacacacaggcctgtgtcggca
ccacctaccaccccgtgctgccctccgtcctcgccacctgctcctggggagggggacatgaagatctggcactgag
cttttgtcactgaaccttcccgatgccagctgggctcttggactcccctcttcctcaagggtagatgagaggaa
cgagcacagaggttggctgtgggtcctgggtaccaccttctgagcctcagtttcctcatctgtaaagtggggaga
aaagtctgtttgcctcaggagtgtgaggactacactagtgaaagcgcctggcgggcagccggcgatgcccaataa
atgtgtgttttgctgtttgttaaaaaaaaaaaaaaaaaaa

**FIG. 3A**

SEQ ID NO:11
MPALCLVLCWFQGLLGEVWNAVDSGHCLQTYSLHTEAVRAARWAPCGRRILSGGFDFALHLTDLETGTQLFSGRS
DFRITTLKFHPKDHNIFLCGGFSSEMKAWDIRTGKVMRSYKATIQQTLDILFLREGSEFLSSTDASTRDSADRTI
IAWDFRTSAKISNQIFHERFTCPSLALHPREPVFLAQTNGNYLALFSTVWPYRMSRRRRYEGHKVEGYSVGCECS
PGGDLLVTGSADGRVLMYSFRTASRACTLQGHTQACVGTTYHPVLPSVLATCSWGGDMKIWH

**FIG. 3B**

```
M          1  -----GAGGGGTGGACCAAGAGCTTCCGTGT-GTGTGTGT-GTGTGGAAGTCAC------
H          1  GGCACGAGGGAGGGAGGCAGGTGAGAGTGATTAGTGCGAGAAGAAAGCAGGCCCAGGACC
consensus  1  .....*****.***.*.*.....*.*.***.*.*..*...*.**.*....*.......

M         48  ---CTTTGTGTGACTGT--ATGGCCTCGCTG-----GTGG--CATATGATG-ATTCTGAC
H         61  AAGCCCTG-GGGACTGGGGACATCCTCGGTGACCCTGTGGAGCATTGAGCCATGCCAGC
consensus 61  ...*..**.*.*****...*.*****.**.....****..***.***..*.**.*..*

M         95  TCCGAGACCGAGGCTGACCCTGCCAGAAGTGGGGACGCTCCAGGTGTGGAATGCTGTGGA
H        119  TCTGTGCCTCGGTGCTGTGCTGGTTTCAAGGGCTGTTGGGAGAGGTATGGAACGCCGTGGA
consensus 121  **.*.*.*.****.*.*.*.***.**.*****.*.*..****.*****.**.*****

M        155  CTCGGGACACTGCCTGCAGACCTACTCTGTGCACAGTGAGGCAGTAAGGGCTGAACGGTG
H        179  CTCCGGGCACTGCCTGCAGACCTACTCCCTGCACACAGAGGCAGTGCGGGCCGCCCGGTG
consensus 181  ***.**.***************.**.******.*.*.*****.****.****.*.****

M        215  GTCTCCCTGTGGCCGGCGCATCCTCAGTGGTGGCTTCGACTTGGCCTGCACCTAACAGA
H        239  GGCTCCCTGTGGCCGGCGCATCCTCAGTGGTGGCTTTGACTTCGCGCTGCACCTAACAGA
consensus 241  *.**********************************.*****.**.************

M        275  CCTTGAAACAGGAACCCAAGTGTTTAGTGGTCAGAGTGACTTCAGAGTCACCACCTTGAA
H        299  CCTTGAAACAGGAACCCAGCTATTTAGTGGTCGAAGTGACTTTAGAATCACTACCTTGAA
consensus 301  ****************..*.*.**********.**.*******..***.****.*******

M        335  ATTTCATCCAAAAGAACACAACGTCTTTTTATGTGGCGGCTTCAGCTCTGAAATCAACAG
H        359  ATTCCATCCAAAAGACCACAACATCTTTTTATGTGGAGGCTTCAGCTCTGAAATGAAAGC
consensus 361  ***.***********.*****.*.************.*****************.**

M        395  GNGGGACATGAGGACTGGCAAGGTGGTGAAAGGCTACAAGGCCACCATCCAGCAGACCCT
H        419  TTGGGATATAAGGACTGGCAAGGTGATGAGAAGCTACAAGGCGACCATCCAGCAGACCTT
consensus 421   .****.**.***********.***.*.*.*********.****************.*

M        455  GGACATTCTCTTCCTCCAGGAGGGCTCCGAGTTTCTTAGCAGTACGGACGCATCCACCCG
H        479  GGACATCCTGTTCCTCCGGGAAGGCTCCGAGTTCCTGAGCAGCACAGACGCTTCCACCCG
consensus 481  ******.**.*******.***.***********.**.*****.**.*****.*.*******

M        515  GGACTCTGCTGACCGAACCATTATCGCCTGGGATTTCCGGACCGCTGCCAAGATCTCCAA
H        539  GGACTCAGCTGACCGCACCATTATTGCCTGGGATTTCCGGACCTCTGCCAAAATCTCCAA
consensus 541  ******.*******.*********.********************.*******.*******

M        575  CCAGATCTTCCATGAGAGGTACACCTGTCCCAGCCTCGCCTTGCATCCAAGGGAGCCTGT
H        599  CCAGATTTTCCACGAGAGGTTCACCTGCCCCAGCCTCGCCTTGCACCCGAGAGAGCCCGT
consensus 601  ******.*****.*******.******.*****************.**.**.*****.**

M        635  GTTCCTTGCACAAAACCAATGGCAACTACCTGGCTCTCTTTTCCTCTGTGTGGCCCTATCG
H        659  GTTCCTGGCACAGACCAATGGCAACTACCTGGCCCTTTTCTCCACTGTGTGGCCCTACCG
consensus 661  ******.*****.*.************************.**.**.************.**

M        695  GATGAGCAGACGGAGAGACGCTACGAAGGTCACAAGGTGGAAGGCTACGCGGTGGGCTGTGA
H        719  GATGAGCAGACGGCGGCGCTATGAAGGCACAAGGTGGAGGGCTACTCAGTGGGCTGCGA
consensus 721  ***********.*.*.*****.*****.************.*****.*.*.*******.**
```

**FIG. 4A**

```
M           755  GTGTTCCCCATGTGGTGACCTGCTGGTGACAGGCAGCGCTGATGGCCGGGTTTTGATGTT
H           779  GTGCTCCCCAGGCGGTGACTTGCTGGTGACGGGCAGCGCCGATGGCCGGGTCCTGATGTA
consensus   781  *** ****** * ****** ********** ******* *********** ******

M           815  CAGTTTCCGCACGGCCAGCCGAGCGTGCGCACTACAAGGGCACACGCAGGCCTGCCTTGG
H           839  CAGCTTCCGCACAGCCAGCCGAGCATGCACACTGCAGGGGCACACACAGGCCTGTGTCGG
consensus   841  *** ******** ************* *** *** ** ******** ******* * **

M           875  CACCAGCTACCATCCTGTGCTGCCTTCTGTCCTCGGGACCTGCTCCTGGGGAGGAGACAT
H           899  CACCACCTACCACCCCGTGCTGCCCTCCGTCCTCGCCACCTGCTCCTGGGGAGGGGACAT
consensus   901  ***** ****** ** ******** ** ******* ***************** *****

M           935  CAAGATCTGGCACT---------------AAC--------TGGCAACTGAGACCTG---
H           959  GAAGATCTGGCACTGAGCTTTTTGTCACTGAACCTTCCCGATGCCAGCTGGGCTCTTGGA
consensus   961  ************* ................***........** ** .*** .*  **...

M           968  --CCCCT----------GGG------ATAGG--CG-GC-CGGAGGTCAGGCTGC---TCCC
H          1019  CTCCCCTCTTCCTCAAGGGTAGATGAGAGGAACGAGCACAGAGGTT-GGCTGTGGGTCGT
consensus  1021  ..******..........***......* ***..**.**.*.***** .***** ...***

M          1004  GAG----AGCTGCTGGGCTTCAGTGAC-TCGGCTATAGCATGGGGTGAGAACGCCGTCT
H          1078  GGGTACCACCTTCTGAGCCTCAGTTTCCTCATCTGTAA-AGTGGGGAGAAAAGTCTGTTT
consensus  1081  *.*....* ** ***.** ***** *.**.** ** ...* **** ** ** * ** *

M          1059  CGGCGCAAGCGTGTGTCAGAACGGGG-TAGCCGAAGTGACTGGTGGGCGA----------
H          1137  -GCCTCAGGAGTGTG--AGGACTACACTAGTGAAAGCGCCTGCCGGGCAGCCGGCGATGC
consensus  1141  .* * **.* *****..**.** . ...*** .*** * **** ****...........

M
H          1194  CCAATAAATGTGTGTTTGCTGTTTGTTAAAAAAAAAAAAAAAAAA
consensus  1201  .............................................
```

FIG. 4A (continued)

```
M           1  MMILTPRPRLTLPEVGTLQVWNAVDSGHCLQTYSVHSEAVRADRWSPCGRRILSGGFDFA
H           1  --MPALCLVLCWFQGLLGEVWNAVDSGHCLQTYSLHTEAVRAARWAPCGRRILSGGFDFA
consensus   1  ...       *        ***************.*.***** ** *************


M          61  LHLTDLETGTQVFSGQSDFRVTTLKFHPKEHNVFLCGGFSSEINRXDMRTGKVVKGYKAT
H          59  LHLTDLETGTQLFSGRSDFRLTTLKFHPKDHNIFLCGGFSSEMKAWDIRTGKVMRSYKAT
consensus  61  ***********.***.****.********.**.*********.    .*.*****.. ****


M         121  IQQTLDILFLQEGSEFLSSTDASTRDSADRTIIAWDFRTAAKISNQIFHERYTCPSLALH
H         119  IQQTLDILFLREGSEFLSSTDASTRDSADRTIIAWDFRTSAKISNQIFHERFTCPSLALH
consensus 121  **********.***********************************.********


M         181  PREPVFLAQTNGNYLALFSSVWPYRMSRRRRYEGHKVEGYAVGCECSPCGDLLVTGSADG
H         179  PREPVFLAQTNGNYLALFSTVWPYRMSRRRRYEGHKVEGYSVGCECSPGGDLLVTGSADG
consensus 181  *******************.********************.******* **********


M         241  RVLMFSFRTASRACALQGHTQACLGTSYHPVLPSVLGTCSWGGDIKIWH
H         239  RVLMYSFRTASRACTLQGHTQACVGTTYHPVLPSVLATCSWGGDMKIWH
consensus 241  ****.*********.********.**.**********.*******.****
```

**FIG. 4B**
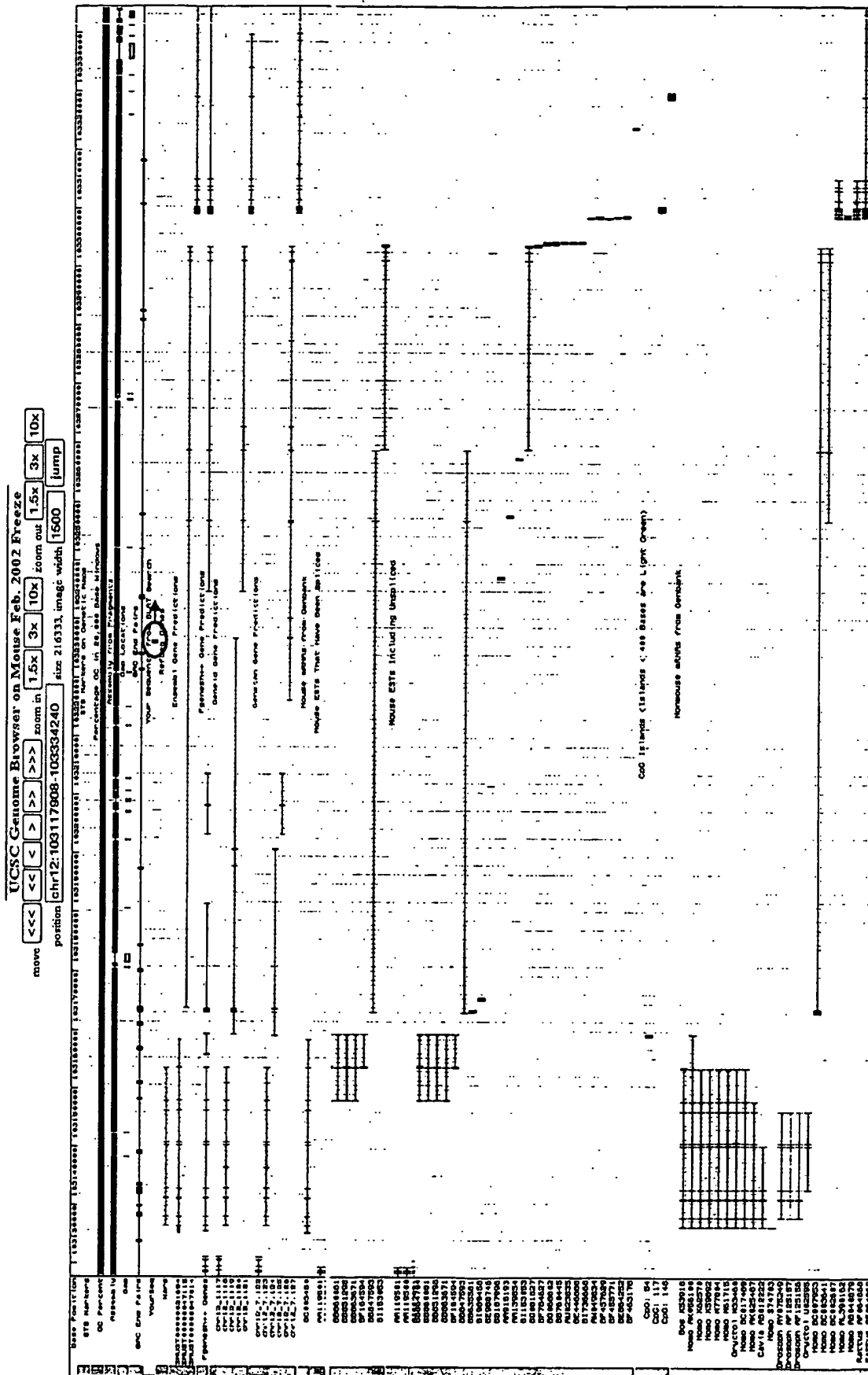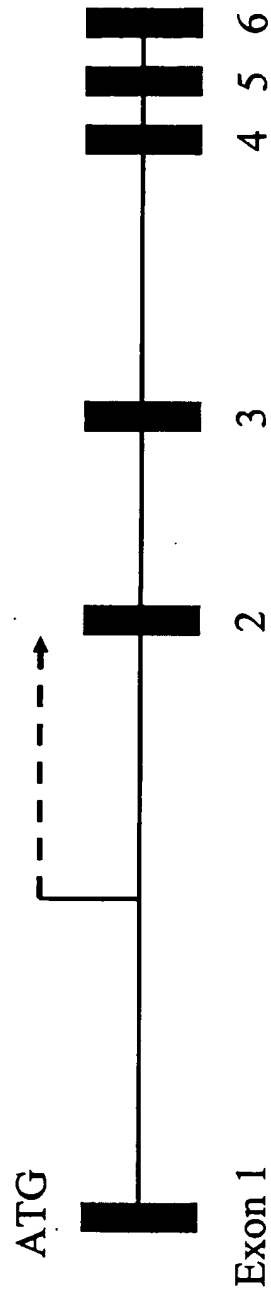
10/524433



FIG.5A

FIG. 5B

10/524433



FIG.6A

# SMART

**S** imple
**M** odular
**A** rchitecture
**R** esearch
**T** ool
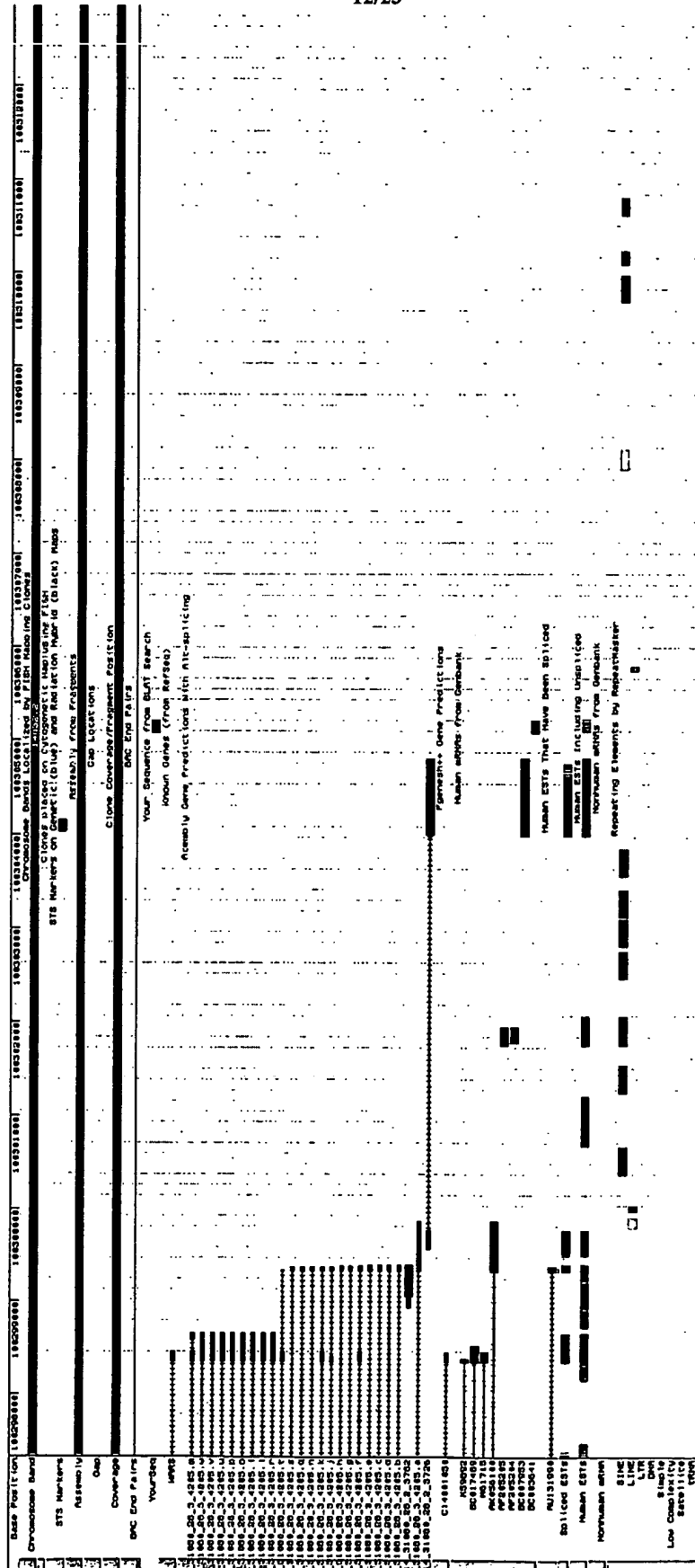
Menu: Schultz et al. (1998) Proc. Natl. Acad. Sci. USA 95, 5857-5864
Letunic et al (2002) Nucleic Acids Res 30, 242-244
HOME| LITERATURE| ABOUT| GLOSSARY| WHATS NEW| FEEDBACK

Currently there are too many SMART jobs running.

Your job is no. 1 in the queue.

Your sequence was 100% identical to sptrembl|Q9BTK5|Q9BTK5, displaying precalculated results.
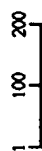
Mouse over domain / undefined region to see the limits; click on it to go to further annotation; right-click to save whole protein as PNG image
Transmembrane segments as predicted by the _THMHMM2_ program (▬▬), coiled coil regions determined by the _Coils2_ program (▬▬) and Segments of low compositional complexity, determined by the _SEG_ program (▬▬)

## Architecture analysis

Display all proteins with similar domain organisation.
Display all proteins with similar domain composition.

Confidently predicted domains, repeats, motifs and features:

| name | begin | end | E-value |
|---|---|---|---|
| Signal peptide | 1 | 17 | . |
| WD40 | 24 | 63 | 4.30e-05 |
| WD40 | 66 | 105 | 1.40e+00 |
| WD40 | 108 | 154 | 1.90e+02 |
| WD40 | 203 | 244 | 3.30e-01 |
| WD40 | 247 | 287 | 2.90e-03 |

The SMART diagram above represents a summary of the results shown below. Domains with scores less significant than established cutoffs are not shown in the diagram. Features are also not shown when two or more occupy the same piece of sequence; the priority for display is given by:
SMART > PFAM > PROSPERO repeats > Signal peptide > Transmembrane > Coiled coil > Low complexity. In either case, features not shown in the above diagram are marked 'hidden'

FIG. 6B

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2 possible models considered, only significant TM-segments used

\*\*\* the models differ in the number of TM-helices ! \*\*\*

----> STRONGLY prefered model: N-terminus inside
2 strong transmembrane helices, total score : 1224
# from  to length score orientation
1   1   21 (21)   510 i-o
2  210  232 (23)   714 o-i

-----> alternative model
1 strong transmembrane helices, total score : 812
# from  to length score orientation
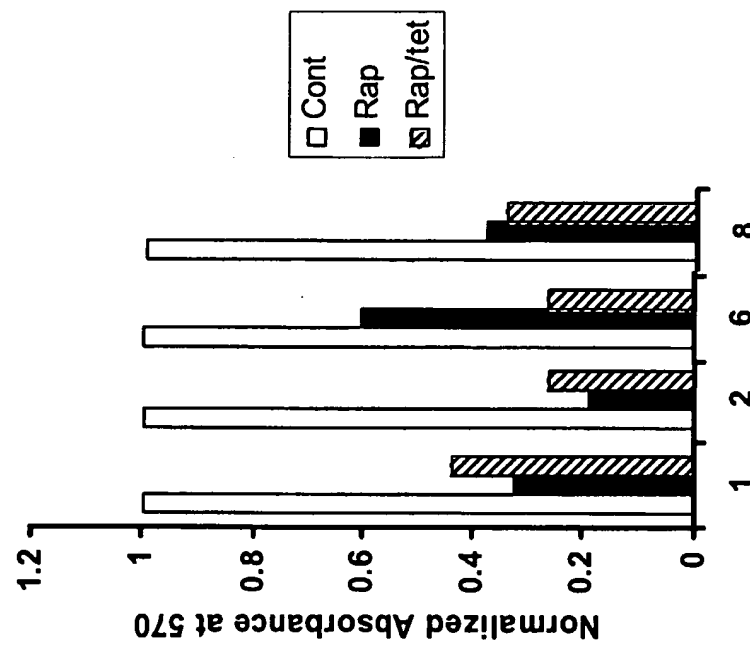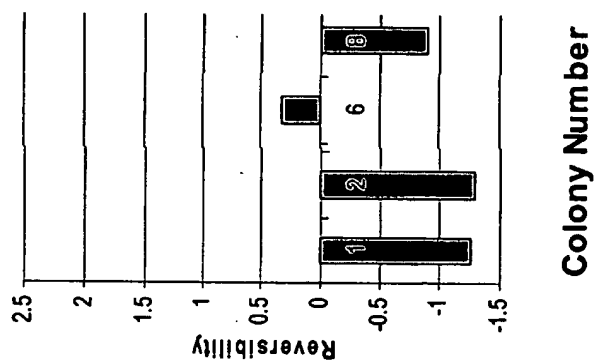1   6   25 (20)   812 o-i
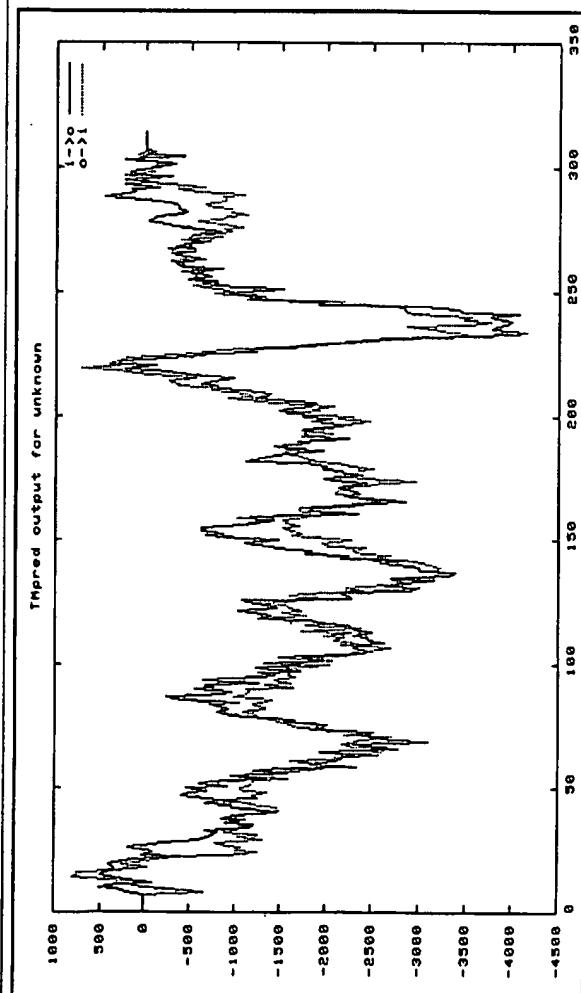


FIG.6C

FIG. 7

FIG. 8A

**Colony Number**

**FIG. 8B**

FIG. 8C

FIG. 8D

FIG. 8E

21/23

FIG. 9A

FIG. 9B

10/524433

GSS-PuroV4



FIG. 9C

Tet-Off System

tTA
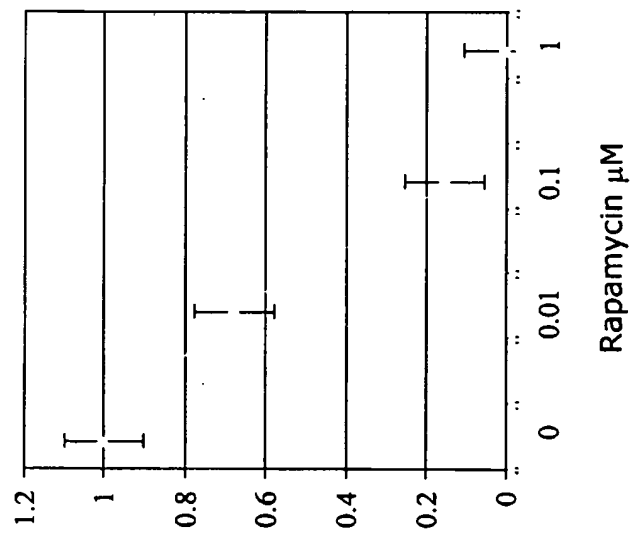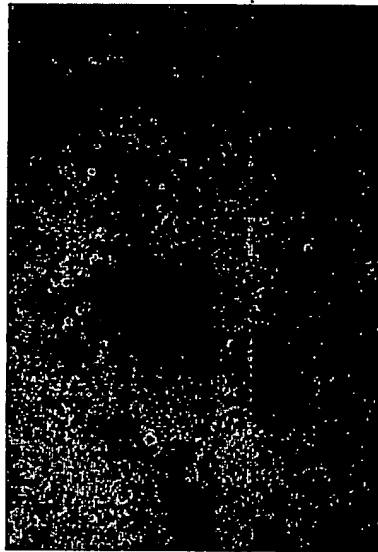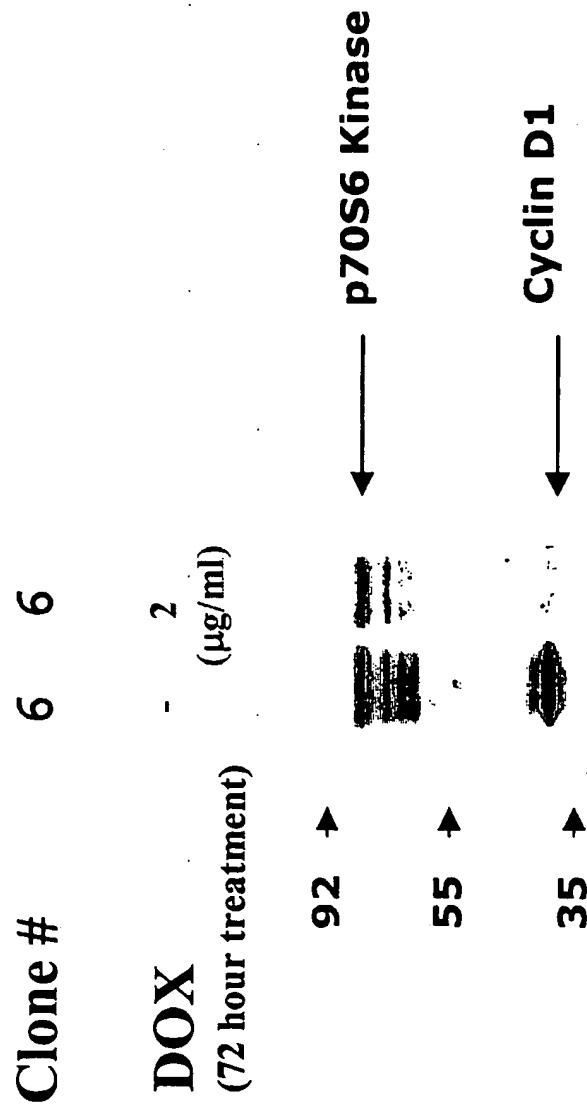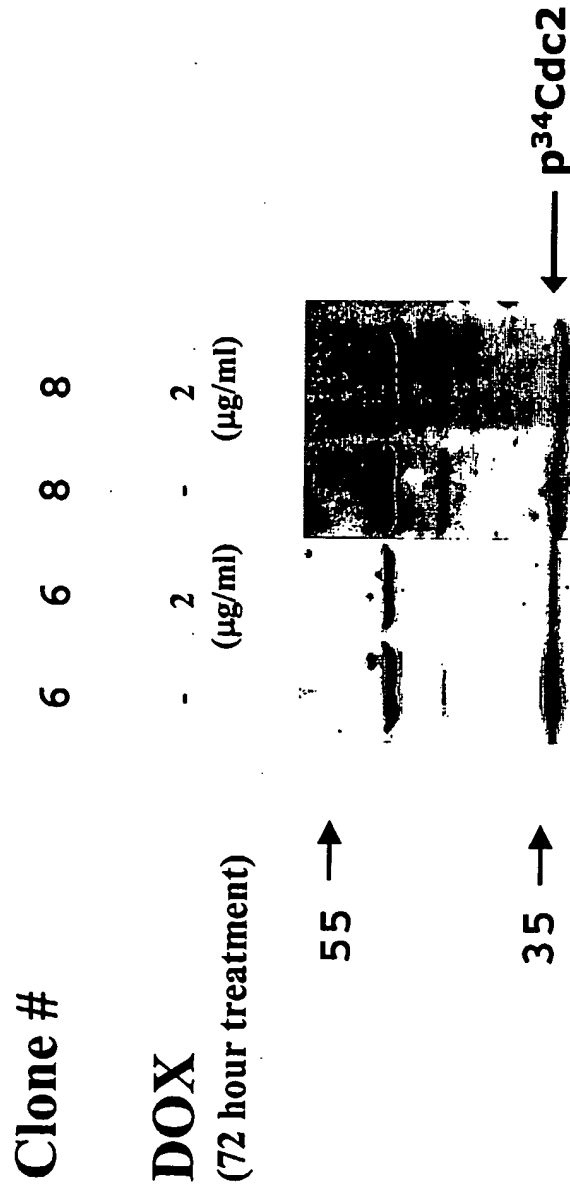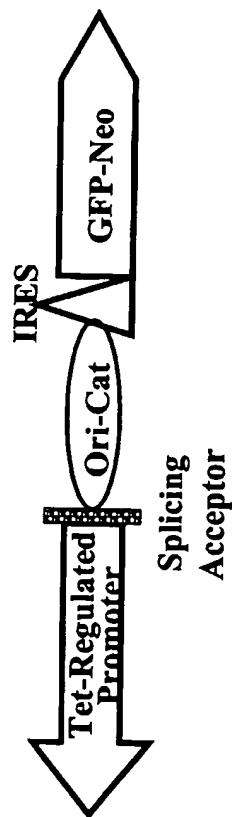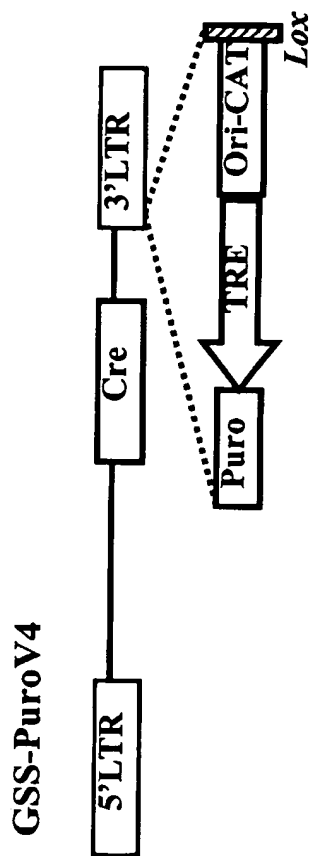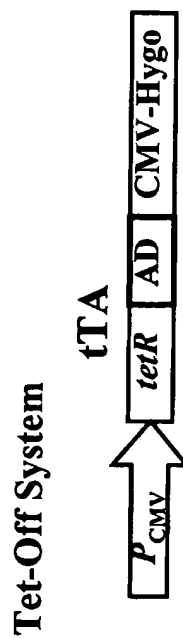


FIG. 9D

| Accession Class | Nucleotide accession | Nucleotide Position | Strand orientation | dbSNP rs# (cluster id) | Protein accession | Function |
|---|---|---|---|---|---|---|
| NCBI RefSeq | NM_024515.1 | 908 | minus strand | rs13065 | NP_078791.1 | unclassified |
| | | 1192 | minus strand | rs13492 | NP_078791.1 | unclassified |
| GenBank mRNA | BC003641.1 | 908 | minus strand | rs13065 | AAH03641.1 | unclassified |
| | | 1192 | minus strand | rs13492 | AAH03641.1 | unclassified |

FIG.10